RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/573,166_____

Source: _____ JFWOP_____

Date Processed by STIC: _____ 04/10/2006_____

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IFWP

RAW SEQUENCE LISTING   DATE: 04/10/2006
PATENT APPLICATION: US/10/573,166   TIME: 10:42:20

Input Set : A:\P2610US_SEQ ST25.txt
Output Set: N:\CRF4\04102006\J573166.raw

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 3 <110> APPLICANT: Tanaka, Akito
 4         Yamazaki, Akira
 5         Tsutsumi, Takeshi
 6         Terada, Tomohiro
 7         Haramura, Masayuki
 9 <120> TITLE OF INVENTION: NOVEL TARGET PROTEIN OF ANTICANCER AGENT AND NOVEL
ANTICANCER
10        AGENT (SPNAL) CORRESPONDING THERETO
12 <130> FILE REFERENCE: P2610US
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C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/573,166
C--> 14 <141> CURRENT FILING DATE: 2006-03-21
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14 <150> PRIOR APPLICATION NUMBER: JP 2003-401132
15 <151> PRIOR FILING DATE: 2003-12-01
17 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/018108
18 <151> PRIOR FILING DATE: 2004-11-30
20 <160> NUMBER OF SEQ ID NOS: 3
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3009
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (94)..(2229)
32 <223> OTHER INFORMATION:
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38 cagcctccgc gccaggcccg gccccgccgc gcc atg tcg gac tac agc acg gga    114
39                                     Met Ser Asp Tyr Ser Thr Gly
40                                       1           5
42 gga ccc ccg ccc ggg ccg ccg ccg ccc gcc ggc ggg ggc ggg gga gcc    162
43 Gly Pro Pro Pro Gly Pro Pro Pro Pro Ala Gly Gly Gly Gly Gly Ala
44       10              15                  20
46 gga ggc gcc ggg gga ggc cct ccg ccg ggc ccg cca ggc gcg ggg gac    210
47 Gly Gly Ala Gly Gly Gly Pro Pro Pro Gly Pro Pro Gly Ala Gly Asp
48       25              30                  35
50 cgg ggc ggc ggc ggt ccc tgc ggc ggc ggc ccg ggc ggg ggg tcg gcc    258
51 Arg Gly Gly Gly Gly Pro Cys Gly Gly Gly Pro Gly Gly Gly Ser Ala
52 40              45                  50                  55
54 ggg ggc ccc tct cag cca ccc ggc gga ggc ggc ccg gga atc cgc aag    306
55 Gly Gly Pro Ser Gln Pro Pro Gly Gly Gly Gly Pro Gly Ile Arg Lys
56              60                  65                  70
58 gac gct ttc gcc gac gcc gtg cag cgg gcc cgc cag att gca gcc aaa    354
59 Asp Ala Phe Ala Asp Ala Val Gln Arg Ala Arg Gln Ile Ala Ala Lys
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60              75                  80                  85
62 att gga ggc gat gct gcc acg aca gtg aat aac agc act cct gat ttt      402
63 Ile Gly Gly Asp Ala Ala Thr Thr Val Asn Asn Ser Thr Pro Asp Phe
64         90                  95                  100
66 ggt ttt ggg ggc caa aag aga cag ttg gaa gat gga gat caa ccg gag      450
67 Gly Phe Gly Gly Gln Lys Arg Gln Leu Glu Asp Gly Asp Gln Pro Glu
68     105                 110                 115
70 agc aag aag ctg gct tcc cag gga gac tca atc agt tct caa ctt gga      498
71 Ser Lys Lys Leu Ala Ser Gln Gly Asp Ser Ile Ser Ser Gln Leu Gly
72 120                 125                 130                 135
74 ccc atc cat cct ccc cca agg act tca atg aca gaa gag tac agg gtc      546
75 Pro Ile His Pro Pro Pro Arg Thr Ser Met Thr Glu Glu Tyr Arg Val
76                 140                 145                 150
78 cca gac ggc atg gtg ggc ctg atc att ggc aga gga ggt gaa caa att      594
79 Pro Asp Gly Met Val Gly Leu Ile Ile Gly Arg Gly Gly Glu Gln Ile
80             155                 160                 165
82 aac aaa atc caa cag gat tca ggc tgc aaa gta cag att tct cca gac      642
83 Asn Lys Ile Gln Gln Asp Ser Gly Cys Lys Val Gln Ile Ser Pro Asp
84         170                 175                 180
86 agc ggt ggc cta ccc gag cgc agt gtg tcc ttg aca gga gcc cca gaa      690
87 Ser Gly Gly Leu Pro Glu Arg Ser Val Ser Leu Thr Gly Ala Pro Glu
88     185                 190                 195
90 tct gtc cag aaa gcc aag atg atg ctg gat gac att gtg tct cgg ggt      738
91 Ser Val Gln Lys Ala Lys Met Met Leu Asp Asp Ile Val Ser Arg Gly
92 200                 205                 210                 215
94 cgt ggg ggc ccc cca gga cag ttc cac gac aac gcc aac ggg ggc cag      786
95 Arg Gly Gly Pro Pro Gly Gln Phe His Asp Asn Ala Asn Gly Gly Gln
96             220                 225                 230
98 aac ggc acc gtg cag gag atc atg atc ccc gcg ggc aag gcc ggc ctg      834
99 Asn Gly Thr Val Gln Glu Ile Met Ile Pro Ala Gly Lys Ala Gly Leu
100             235                 240                 245
102 gtc att ggc aag ggc ggg gag acc att aag cag ctg cag gaa cgc gct      882
103 Val Ile Gly Lys Gly Gly Glu Thr Ile Lys Gln Leu Gln Glu Arg Ala
104         250                 255                 260
106 gga gtg aag atg atc tta att cag gac gga tct cag aat acg aat gtg      930
107 Gly Val Lys Met Ile Leu Ile Gln Asp Gly Ser Gln Asn Thr Asn Val
108     265                 270                 275
110 gac aaa cct ctc cgc atc att ggg gat cct tac aaa gtg cag caa gcc      978
111 Asp Lys Pro Leu Arg Ile Ile Gly Asp Pro Tyr Lys Val Gln Gln Ala
112 280                 285                 290                 295
114 tgt gag atg gtg atg gac atc ctc cgg gaa cgt gac caa ggc ggc ttt      1026
115 Cys Glu Met Val Met Asp Ile Leu Arg Glu Arg Asp Gln Gly Gly Phe
116             300                 305                 310
118 ggg gac cgg aat gag tac gga tct cgg att ggc gga ggc atc gat gtg      1074
119 Gly Asp Arg Asn Glu Tyr Gly Ser Arg Ile Gly Gly Gly Ile Asp Val
120             315                 320                 325
122 cca gtg ccc agg cat tct gtt ggc gtg gtc att ggc cgg agt gga gag      1122
123 Pro Val Pro Arg His Ser Val Gly Val Val Ile Gly Arg Ser Gly Glu
124             330                 335                 340
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126 atg atc aag aag atc cag aat gat gct ggc gtg cgg ata cag ttc aag   1170
127 Met Ile Lys Lys Ile Gln Asn Asp Ala Gly Val Arg Ile Gln Phe Lys
128     345             350             355
130 caa gat gac ggg aca ggg ccc gag aag att gct cat ata atg ggg ccc   1218
131 Gln Asp Asp Gly Thr Gly Pro Glu Lys Ile Ala His Ile Met Gly Pro
132 360             365             370                 375
134 cca gac agg tgc gag cac gca gcc cgg atc atc aac gac ctc ctc cag   1266
135 Pro Asp Arg Cys Glu His Ala Ala Arg Ile Ile Asn Asp Leu Leu Gln
136             380             385             390
138 agc ctc agg agt ggt ccc cca ggt cct cca ggg ggt cca ggc atg ccc   1314
139 Ser Leu Arg Ser Gly Pro Pro Gly Pro Pro Gly Gly Pro Gly Met Pro
140             395             400             405
142 ccg ggg ggc cga ggc cga gga aga ggc caa ggc aat tgg ggt ccc cct   1362
143 Pro Gly Gly Arg Gly Arg Gly Arg Gly Gln Gly Asn Trp Gly Pro Pro
144             410             415             420
146 ggc ggg gag atg acc ttc tcc atc ccc act cac aag tgt ggg ctg gtc   1410
147 Gly Gly Glu Met Thr Phe Ser Ile Pro Thr His Lys Cys Gly Leu Val
148     425             430             435
150 atc ggc cga ggt ggc gag aat gtg aaa gcc ata aac cag cag acg gga   1458
151 Ile Gly Arg Gly Gly Glu Asn Val Lys Ala Ile Asn Gln Gln Thr Gly
152 440             445             450             455
154 gcc ttc gta gag atc tcc cgg cag ctg cca ccc aac ggg gac ccc aac   1506
155 Ala Phe Val Glu Ile Ser Arg Gln Leu Pro Pro Asn Gly Asp Pro Asn
156             460             465             470
158 ttc aag ttg ttc atc atc cgg ggt tca ccc cag cag att gac cac gcc   1554
159 Phe Lys Leu Phe Ile Ile Arg Gly Ser Pro Gln Gln Ile Asp His Ala
160             475             480             485
162 aag cag ctt atc gag gaa aag atc gag ggt cct ctc tgc cca gtt gga   1602
163 Lys Gln Leu Ile Glu Glu Lys Ile Glu Gly Pro Leu Cys Pro Val Gly
164             490             495             500
166 cca ggc cca ggt ggc cca ggc cct gct ggc cca atg ggg ccc ttc aat   1650
167 Pro Gly Pro Gly Gly Pro Gly Pro Ala Gly Pro Met Gly Pro Phe Asn
168     505             510             515
170 cct ggg ccc ttc aac cag ggg cca ccc ggg gct ccc cca cat gcc ggg   1698
171 Pro Gly Pro Phe Asn Gln Gly Pro Pro Gly Ala Pro Pro His Ala Gly
172 520             525             530                 535
174 ggg ccc cct cct cac cag tac cca ccc cag ggc tgg ggc aat acc tac   1746
175 Gly Pro Pro Pro His Gln Tyr Pro Pro Gln Gly Trp Gly Asn Thr Tyr
176             540             545             550
178 ccc cag tgg cag ccg cct gct cct cat gac cca agc aaa gca gct gca   1794
179 Pro Gln Trp Gln Pro Pro Ala Pro His Asp Pro Ser Lys Ala Ala Ala
180             555             560             565
182 gcg gcc gcg gac ccc aac gcc gcg tgg gcc gcc tac tac tca cac tac   1842
183 Ala Ala Ala Asp Pro Asn Ala Ala Trp Ala Ala Tyr Tyr Ser His Tyr
184             570             575             580
186 tac cag cag ccc ccg ggc ccc gtc ccc ggc ccc gca ccg gcc cct gcg   1890
187 Tyr Gln Gln Pro Pro Gly Pro Val Pro Gly Pro Ala Pro Ala Pro Ala
188     585             590             595
190 gcc cca ccg gct cag ggt gag ccc cct cag ccc cca ccc acc ggc cag   1938
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191 Ala Pro Pro Ala Gln Gly Glu Pro Pro Gln Pro Pro Pro Thr Gly Gln
192 600             605             610             615
194 tcg gac tac act aag gcc tgg gaa gag tat tac aaa aag atc ggc cag       1986
195 Ser Asp Tyr Thr Lys Ala Trp Glu Glu Tyr Tyr Lys Lys Ile Gly Gln
196             620             625             630
198 cag ccc cag cag ccc gga gcg ccc cca cag cag gac tac acg aag gct       2034
199 Gln Pro Gln Gln Pro Gly Ala Pro Pro Gln Gln Asp Tyr Thr Lys Ala
200             635             640             645
202 tgg gag gag tac tac aag aag caa gcg caa gtg gcc acc gga ggg ggt       2082
203 Trp Glu Glu Tyr Tyr Lys Lys Gln Ala Gln Val Ala Thr Gly Gly Gly
204             650             655             660
206 cca gga gct ccc cca ggc tcc cag cca gac tac agt gcc gcc tgg gcg       2130
207 Pro Gly Ala Pro Pro Gly Ser Gln Pro Asp Tyr Ser Ala Ala Trp Ala
208         665             670             675
210 gaa tat tac aga cag cag gcc gct tac tac gga cag acc cca ggt cct       2178
211 Glu Tyr Tyr Arg Gln Gln Ala Ala Tyr Tyr Gly Gln Thr Pro Gly Pro
212 680             685             690             695
214 ggc ggc ccc cag ccg ccg ccc acg cag cag gga cag cag cag gct caa       2226
215 Gly Gly Pro Gln Pro Pro Pro Thr Gln Gln Gly Gln Gln Gln Ala Gln
216             700             705             710
218 tga atcgaatgaa tgtgaacttc ttcatctgtg aaaaatcttt tttttttcca            2279
220 ttttgttctg tttgggggct tctgttttgt ttggcgagag agcgatggtg ccgtgggggag     2339
222 tactggggag ccctcgcggc aagcagggtg ggggggactt ggggggcatgc cgggccctca     2399
224 ctctctcgcc tgttctgtgt ctcacatgct ttttctttca aaattgggat ccttccatgt      2459
226 tgagccagcc agagaagata gcgagatcta aatctctgcc aaaaaaaaaa aaaacttaaa      2519
228 aattaaaaac acaaagagca aagcagaact tataaaatta tatatatata tattaaaaag      2579
230 tctctattct tcacccccca gccttcctga acctgcctct ctgaggataa agcaattcat      2639
232 tttctcccac cctcggccct cttgttttta aaataaactt ttaaaaagga aaaaaaaaag      2699
234 tcactcttgc tatttctttt ttttagttag aggtggaaca ttccttggac caggtgttgt      2759
236 attgcaggac ccccttcccc agcagccaag cccctcttc tctccctccc gccctggctc       2819
238 agctcccgcg gccccgcccg tcccccctcc caggactggt ctgttgtctt ttcatctgtt      2879
240 caagaggaga ttgaaactga aaacaaatg agaacaacaa aaaaaattgt atggcagttt       2939
242 ttacttttta tcgctcgttt ttaacttcac aaataaatga taacaaaacc tcaaaaaaaa      2999
244 aaaaaaaaaa                                                            3009
247 <210> SEQ ID NO: 2
248 <211> LENGTH: 711
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
252 <400> SEQUENCE: 2
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258 Ala Gly Gly Gly Gly Gly Ala Gly Gly Ala Gly Gly Gly Pro Pro Pro
259             20              25              30
262 Gly Pro Pro Gly Ala Gly Asp Arg Gly Gly Gly Gly Pro Cys Gly Gly
263         35              40              45
266 Gly Pro Gly Gly Gly Ser Ala Gly Gly Pro Ser Gln Pro Pro Gly Gly
267     50              55              60
270 Gly Gly Pro Gly Ile Arg Lys Asp Ala Phe Ala Asp Ala Val Gln Arg
271 65              70              75              80
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274 Ala Arg Gln Ile Ala Ala Lys Ile Gly Gly Asp Ala Ala Thr Thr Val
275              85                90                95
278 Asn Asn Ser Thr Pro Asp Phe Gly Phe Gly Gly Gln Lys Arg Gln Leu
279             100             105             110
282 Glu Asp Gly Asp Gln Pro Glu Ser Lys Lys Leu Ala Ser Gln Gly Asp
283         115             120             125
286 Ser Ile Ser Ser Gln Leu Gly Pro Ile His Pro Pro Pro Arg Thr Ser
287     130             135             140
290 Met Thr Glu Glu Tyr Arg Val Pro Asp Gly Met Val Gly Leu Ile Ile
291 145             150             155             160
294 Gly Arg Gly Gly Glu Gln Ile Asn Lys Ile Gln Gln Asp Ser Gly Cys
295             165             170             175
298 Lys Val Gln Ile Ser Pro Asp Ser Gly Gly Leu Pro Glu Arg Ser Val
299             180             185             190
302 Ser Leu Thr Gly Ala Pro Glu Ser Val Gln Lys Ala Lys Met Met Leu
303         195             200             205
306 Asp Asp Ile Val Ser Arg Gly Arg Gly Gly Pro Pro Gly Gln Phe His
307     210             215             220
310 Asp Asn Ala Asn Gly Gly Gln Asn Gly Thr Val Gln Glu Ile Met Ile
311 225             230             235             240
314 Pro Ala Gly Lys Ala Gly Leu Val Ile Gly Lys Gly Gly Glu Thr Ile
315             245             250             255
318 Lys Gln Leu Gln Glu Arg Ala Gly Val Lys Met Ile Leu Ile Gln Asp
319         260             265             270
322 Gly Ser Gln Asn Thr Asn Val Asp Lys Pro Leu Arg Ile Ile Gly Asp
323         275             280             285
326 Pro Tyr Lys Val Gln Gln Ala Cys Glu Met Val Met Asp Ile Leu Arg
327     290             295             300
330 Glu Arg Asp Gln Gly Gly Phe Gly Asp Arg Asn Glu Tyr Gly Ser Arg
331 305             310             315             320
334 Ile Gly Gly Gly Ile Asp Val Pro Val Pro Arg His Ser Val Gly Val
335             325             330             335
338 Val Ile Gly Arg Ser Gly Glu Met Ile Lys Lys Ile Gln Asn Asp Ala
339             340             345             350
342 Gly Val Arg Ile Gln Phe Lys Gln Asp Asp Gly Thr Gly Pro Glu Lys
343         355             360             365
346 Ile Ala His Ile Met Gly Pro Pro Asp Arg Cys Glu His Ala Ala Arg
347     370             375             380
350 Ile Ile Asn Asp Leu Leu Gln Ser Leu Arg Ser Gly Pro Pro Gly Pro
351 385             390             395             400
354 Pro Gly Gly Pro Gly Met Pro Pro Gly Gly Arg Gly Arg Gly Arg Gly
355             405             410             415
358 Gln Gly Asn Trp Gly Pro Pro Gly Gly Glu Met Thr Phe Ser Ile Pro
359             420             425             430
362 Thr His Lys Cys Gly Leu Val Ile Gly Arg Gly Gly Glu Asn Val Lys
363         435             440             445
366 Ala Ile Asn Gln Gln Thr Gly Ala Phe Val Glu Ile Ser Arg Gln Leu
367     450             455             460
370 Pro Pro Asn Gly Asp Pro Asn Phe Lys Leu Phe Ile Ile Arg Gly Ser
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VERIFICATION SUMMARY   DATE: 04/10/2006
PATENT APPLICATION: **US/10/573,166**   TIME: 10:42:21

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:32